



SEQUENCE LISTING

<110> Merck & Co., Inc.

LaMonica, Nicola

Facciabene, Andrea

Aurismicchio, Luigi

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND
USES THEREOF

<130> ITR0073YP

<140> 10/589,180

<141> 2006-08-11

<150> PCT/EP2005/001114

<151> 2005-02-03

<150> 60/635,791

<151> 2004-12-14

<150> 60/543,649

<151> 2004-02-11

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<213> Artificial Sequence

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<212> DNA

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<223> CEA-LTA fusion

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<210> 8

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 8

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Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
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Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
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Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
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Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
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Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys
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Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
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Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
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Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		
245	250	255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg		
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Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr		
370	375	380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser		
385	390	395
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn		
420	425	430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser		
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Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile		
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	675	680	685
Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met			
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Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile			
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Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr			
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Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser Leu Arg Ser Ala His Leu			
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Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val			
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Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val			

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Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe		830
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Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala		845
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Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys		860
865	870	875
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<210> 9

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<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 9

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<213> Artificial Sequence

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<223> CEA-LTB fusion

<400> 10

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Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35             40             45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50             55             60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65             70             75             80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
      85             90             95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
      100            105            110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
      115            120            125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130            135            140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145            150            155            160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
      165            170            175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
      180            185            190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
      195            200            205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
      210            215            220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225            230            235            240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn

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Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala				
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Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile				
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Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn				
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Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro				
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Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln				
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Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
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Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
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Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu			
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Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe			
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Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile			
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Thr Val Ser Ala Ser Gly Thr Leu Asp Ala Pro Gln Ser Ile Thr Glu			
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Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile			
705	710	715	720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser			
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Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr			
	740	745	750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val			
	755	760	765
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<210> 11

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAopt-LTB fusion

<400> 11

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cccagcccc agtacagctg gcgcatcaac ggcatcccc agcagcacac ccaggtgctg 1920
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ataaatgaca agatactatc atatacggaa tcgatggcag gcaaaagaga aatgggttatc 2160
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tcccagaaaa aagccattga aaggatgaag gacacattaa gaatcacata tctgaccgag 2280
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agtatggaaa actag 2355
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<210> 12

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 12

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accccccttca acgtggccga gggcaaggag gtgctgctgc tgggtgcacaa cctgccccag 180
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taccgccagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccggt ggaggacaag 480
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agcatggaga attgataa                                     2358

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<210> 13

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 13

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
  1             5             10             15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20             25             30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35             40             45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly

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50	55	60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile		
65	70	75
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser		80
	85	90
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile		95
	100	105
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp		110
	115	120
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		125
	130	135
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		140
145	150	155
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr		160
	165	170
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln		175
	180	185
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn		190
	195	200
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		205
	210	215
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		220
225	230	235
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		240
	245	250
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		255
	260	265
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		270
	275	280
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		285
	290	295
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		300
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		320
	325	330
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		335
	340	345
		350

- 17 -

	645		650		655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile					
	660		665		670
Thr Val Ser Ala Ser Gly Thr Ser Arg Ala Pro Gln Ser Ile Thr Glu					
	675		680		685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys					
	690		695		700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile					
705		710		715	720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser					
	725		730		735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr					
	740		745		750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val					
	755		760		765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn					
	770		775		780

<210> 14

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 14

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cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccaaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
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gacgccgtgg ccctgacctg cgagcccag acccaggaca ccacctacct gtggtgggtg 540

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accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
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agcatggaga attgataa

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2358

<210> 15

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 15

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Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
          20           25           30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
          35           40           45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
          50           55           60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65           70           75           80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
          85           90           95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
          100          105          110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
          115          120          125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
          130          135          140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145           150           155           160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
          165          170          175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
          180          185          190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
          195          200          205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
          210          215          220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225           230           235           240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
          245          250          255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe

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260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu		
325	330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg		
355	360	365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro		
370	375	380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser		
385	390	395
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn		
420	425	430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser		
435	440	445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile		
450	455	460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His		
465	470	475
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val		
485	490	495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro		
500	505	510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu		
515	520	525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser		
530	535	540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser		
545	550	555
		560

Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser			
	565	570	575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly			
	580	585	590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly			
	595	600	605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln			
	610	615	620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu			
	625	630	635
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe			
	645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile			
	660	665	670
Ser Val Ser Ser Gly Asp Ser Ser Arg Ala Pro Gln Ser Ile Thr Glu			
	675	680	685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys			
	690	695	700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile			
	705	710	715
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser			
	725	730	735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr			
	740	745	750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val			
	755	760	765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn			
	770	775	780

<210> 16

<211> 2118

<212> DNA

<213> Macaca mulatta

<400> 16

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<211> 2118

<212> DNA

<213> *Macaca mulatta*

<400> 17

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<210> 18

<211> 705

<212> PRT

<213> Macaca mulatta

<400> 18

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			20					25					30		
Thr	Ala	Gln	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
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Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly
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Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly
65				70					75					80	
Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser
			85					90					95		
Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val
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Thr	Gln	Ser	Asp	Thr	Gly	Ser	Tyr	Thr	Ile	Gln	Val	Ile	Lys	Glu	Asp
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	130					135					140				
Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys
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Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Glu
		180						185					190		
Leu	Ser	Ser	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	Arg	Asn
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Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
                      260                      265                      270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
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Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
                      290                      295                      300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
  305                      310                      315                      320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
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Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
                      340                      345                      350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
                      355                      360                      365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
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Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
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Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
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Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
                      420                      425                      430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
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Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
                      450                      455                      460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
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Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
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Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro

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[illegible]

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<210> 19
<211> 705
<212> PRT
<213> Macaca mulatta
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Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35                      40                      45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
      50                      55                      60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65                      70                      75                      80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
      85                      90                      95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
      100                      105                      110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
      115                      120                      125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130                      135                      140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                      150                      155                      160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
      165                      170                      175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
      180                      185                      190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
      195                      200                      205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
      210                      215                      220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                      230                      235                      240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
      245                      250                      255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
      260                      265                      270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
      275                      280                      285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
      290                      295                      300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala

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Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu			
325	330	335	
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr			
340	345	350	
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg			
355	360	365	
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro			
370	375	380	
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser			
385	390	395	400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn			
420	425	430	
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Phe			
435	440	445	
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile			
450	455	460	
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His			
465	470	475	480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val			
485	490	495	
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro			
500	505	510	
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser			
545	550	555	560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser			
565	570	575	
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly			
595	600	605	

Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
610 615 620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625 630 635 640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
645 650 655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
660 665 670
Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
675 680 685
Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
690 695 700
Met
705

<210> 20
<211> 702
<212> PRT
<213> Homo sapiens

<400> 20
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35 40 45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp

115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln		
180	185	190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn		
195	200	205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		
210	215	220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		
245	250	255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg		
355	360	365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr		
370	375	380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser		
385	390	395
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415

Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn
			420					425					430		
Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser
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Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile
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Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn
465					470					475				480	
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val
				485					490				495		
Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro
		500						505					510		
Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln
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Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser
	530					535					540				
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn
545				550					555					560	
Val	Thr	Arg	Asn	Asp	Ala	Arg	Ala	Tyr	Val	Cys	Gly	Ile	Gln	Asn	Ser
			565					570				575			
Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly
		580						585				590			
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly
	595					600						605			
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln
	610					615						620			
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu
625				630						635				640	
Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe
			645						650				655		
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile
		660						665				670			
Thr	Val	Ser	Ala	Ser	Gly	Thr	Ser	Pro	Gly	Leu	Ser	Ala	Gly	Ala	Thr
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<210> 21

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAoptDOMopt fusion

<400> 21

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<210> 22

<211> 2037

<212> DNA

<213> Artificial Sequence

<220>

<223> deleted human CEA

<400> 22

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<210> 23

<211> 679

<212> PRT

<213> Artificial Sequence

<220>

<223> deleted human CEA

<400> 23

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Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35           40           45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50           55           60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65           70           75           80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
      85           90           95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
      100           105           110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
      115           120           125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130           135           140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145           150           155           160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
      165           170           175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
      180           185           190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
      195           200           205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
      210           215           220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225           230           235           240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
      245           250           255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
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Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
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Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
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Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
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Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
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Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
  385                      390                      395                      400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                      405                      410                      415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
                      420                      425                      430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
                      435                      440                      445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
                      450                      455                      460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
  465                      470                      475                      480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                      485                      490                      495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
                      500                      505                      510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
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Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
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Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
  545                      550                      555                      560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
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Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly

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Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
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          610              615              620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
          625              630              635              640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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<210> 24

<211> 3426

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FRC fusion

<400> 24

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<210> 25

<211> 2664

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 25

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<211> 2167

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LAMP fusion

<400> 26

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<210> 27

<211> 3921

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-HSP70 fusion

<400> 27

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3921

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<211> 3585

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-VSVG fusion

<400> 28

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<210> 29

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 29

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36

<210> 30

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 30

gcggcgcgcta gaatcatttg tccatccttc atc

33

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 31

tattctagat tcaacaccaa ttccattttc ttattc

36

<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 32

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36

<210> 33

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 33

tctagataaa actcacacat gccca

25

<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 34

gccgactcat ttacccggag acagggag

28

<210> 35

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 35

tctagatttg atccccattg ctgtgggcgg tgccctg

37

<210> 36

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 36

ggcgtgactc ctcttcctgc caatgaggta ggcaatgag

39

<210> 37

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 37

atatctagat ttcacccatag tttttccaca caacc

35

<210> 38

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 38

gcggcgcct tccttccaag tcggttcac tctatg

36

<210> 39

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 39

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<210> 40

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> PCR Primer, chemically synthesized

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<212> DNA

<213> Artificial Sequence

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<223> PCR Primer, chemically synthesized

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gttatctaga agcaccacca tccc

24

<210> 42

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

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ttaagatctc taagatctgg tgcgtatct cagggg

36

<210> 43

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 43

ttatctagaa agaccacac ctgccccct tgc

33

<210> 44

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 44

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31

<210> 45

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-Dom fusion

<400> 45

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1

5

10

15

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 20 25 30
 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala

305	310	315	320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu			
325	330	335	
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr			
340	345	350	
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg			
355	360	365	
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr			
370	375	380	
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser			
385	390	395	400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn			
420	425	430	
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser			
435	440	445	
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile			
450	455	460	
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn			
465	470	475	480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val			
485	490	495	
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro			
500	505	510	
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn			
545	550	555	560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
565	570	575	
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly			
595	600	605	

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln			
610	615	620	
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu			
625	630	635	640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe			
645	650	655	
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile			
660	665	670	
Thr Val Ser Ala Ser Gly Thr Ser Arg Ser Thr Pro Ile Pro Phe Ser			
675	680	685	
Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp			
690	695	700	
Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp			
705	710	715	720
Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro			
725	730	735	
Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val			
740	745	750	
Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu			
755	760	765	
Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val			
770	775	780	
Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr			
785	790	795	800
Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly			
805	810	815	
Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp			
820	825	830	
Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys			
835	840	845	
Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn			
850	855	860	
Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly			
865	870	875	880
Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile			
885	890	895	
Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile			

900	905	910
Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu		
915	920	925
Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp		
930	935	940
Gly Asn Pro Leu Arg Tyr Asp Thr		
945	950	

<210> 46

<211> 907

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 46

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Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly		
35	40	45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly		
50	55	60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile		
65	70	75
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser		
85	90	95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile		
100	105	110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		

145	150	155	160												
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
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Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln
	180		185		190										
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn
	195		200		205										
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Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
	225		230		235										
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn
	245		250		255										
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe
	260		265		270										
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
	275		280		285										
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser
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Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala
	305		310		315										
Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu
	325		330		335										
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Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg
	355		360		365										
Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr
	370		375		380										
Arg	Asn	Asp	Val	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Glu	Leu	Ser
	385		390		395										
Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp
	405		410		415										
Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn
	420		425		430										
Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser
	435		440		445										

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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 465 470 475 480
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 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
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 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro
 675 680 685
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 690 695 700
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 705 710 715 720
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 725 730 735
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

740	745	750
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val		
755	760	765
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser		
770	775	780
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys		
785	790	795
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp		
805	810	815
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe		
820	825	830
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		
835	840	845
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		
850	855	860
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly		
865	870	875
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
885	890	895
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
900	905	

<210> 47

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> N-terminal domain of fragment C of tetanus toxin

<400> 47

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attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 180
gtgcccggaa taaatggcaa agcaatacat ttagtaaaca atgaatcttc tgaagttata 240
gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgtagcttt 300

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tggttgaggg ttcttaaagt atctgctagt catttagaac aatatggcac aaatgagtat 360
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cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 480
acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 540
actattacta atgatagatt atcttctgct aatttgata taaatggagt acttatggga 600
agtgcagaaa ttactgggtt aggagctatt agagaggata ataataaac attaaaacta 660
gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 720
gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 780
agagacttct ggggaaaccc tttagcatat gatacagata ggtag 825

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<210> 48

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> N-terminal domain of fragment C of tetanus toxin

<400> 48

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          20           25           30
Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe
          35           40           45
Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile
          50           55           60
Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu Val Ile
65           70           75           80
Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe
          85           90           95
Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu
          100          105          110
Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys
          115          120          125
His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn
          130          135          140

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Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile
 145 150 155 160
 Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys
 165 170 175
 Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu
 180 185 190
 Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly
 195 200 205
 Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn
 210 215 220
 Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys
 225 230 235 240
 Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
 245 250 255
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 Asp Arg

<210> 49

<211> 2857

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-DOM fusion

<400> 49

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gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtgggtgggta 540
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agagacttct ggggaaaccc ttacgatat gatatag 2857

<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

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<210> 51

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 51

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1

5

10

15

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Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly		
35	40	45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly		
50	55	60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly		
65	70	75
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser		
85	90	95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val		
100	105	110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu		
180	185	190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn		
195	200	205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg		
210	215	220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn		
245	250	255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
		320

Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Ile	Glu			
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Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr			
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Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	Ser	Arg			
		355					360					365						
Leu	Glu	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro			
	370					375					380							
Arg	Asn	Asp	Thr	Thr	Phe	Tyr	Glu	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser			
385					390					395				400				
Val	Arg	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp			
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Ala	Pro	Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn			
		420					425					430						
Leu	Asn	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Ala	Ala	Gln	Tyr	Ser			
	435					440					445							
Trp	Phe	Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile			
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Pro	Asn	Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His			
465				470					475					480				
Asn	Ser	Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val			
			485				490					495						
Tyr	Val	Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro			
	500						505					510						
Ile	Glu	Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Val	Ala	Glu			
	515						520				525							
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser			
	530					535				540								
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Ile	Leu	Thr	Leu	Leu	Ser			
545				550					555					560				
Val	Thr	Arg	Asn	Asp	Thr	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Ser			
			565					570				575						
Glu	Ser	Ala	Lys	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Thr	Tyr	Gly			
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610	615	620
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625	630	635
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe		640
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Ser Val Ser Ser Gly Asp Ser Ser Arg Ser Thr Pro Ile Pro Phe Ser		
675	680	685
Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp		
690	695	700
Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp		
705	710	715
Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro		720
725	730	735
Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val		
740	745	750
Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu		
755	760	765
Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val		
770	775	780
Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr		
785	790	795
Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly		800
805	810	815
Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp		
820	825	830
Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys		
835	840	845
Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn		
850	855	860
Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly		
865	870	875
Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile		880
885	890	895
Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile		
900	905	910

Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
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<210> 52

<211> 2359

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 52

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agcaaccccg ccgcccagta cagctgggtt gtgaacggca ccttccagca gagcacccag 1380
gagctgttca tccccaacat caccgtgaac aacagcggca gctacatgtg ccaggccac 1440
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cccagcccc agtacagctg gctgatcaac ggcaccctgc gccagcacac ccaggtgctg 1920
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gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040
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agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcgcta cctcaccgag 2280
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<210> 53

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 53

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
  1             5             10             15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20             25             30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35             40             45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly

```

50		55		60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly				
65		70		80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser				
	85		90	95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val				
	100		105	110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp				
	115		120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu				
	130		135	140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys				
145		150		160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr				
	165		170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu				
	180		185	190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn				
	195		200	205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg				
	210		215	220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro				
225		230		240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn				
	245		250	255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe				
	260		265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn				
	275		280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser				
	290		295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala				
305		310		320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu				
	325		330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr				
	340		345	350

```

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
      355                      360                      365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
      370                      375                      380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385                      390                      395                      400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
      405                      410                      415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
      420                      425                      430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
      435                      440                      445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
      450                      455                      460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465                      470                      475                      480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
      485                      490                      495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
      500                      505                      510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
      515                      520                      525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
      530                      535                      540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545                      550                      555                      560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
      565                      570                      575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
      580                      585                      590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
      595                      600                      605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
      610                      615                      620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625                      630                      635                      640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe

```

```

        645                650                655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
        660                665                670
Ser Val Ser Ser Gly Asp Ser Ser Arg Thr Pro Gln Asn Ile Thr Asp
        675                680                685
Leu Cys Ala Glu Tyr His Asn Thr Gln Ile Tyr Thr Leu Asn Asp Lys
        690                695                700
Ile Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile
705                710                715                720
Ile Thr Phe Lys Asn Gly Ala Ile Phe Gln Val Glu Val Pro Gly Ser
        725                730                735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
        740                745                750
Leu Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val
        755                760                765
Trp Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
        770                775                780

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<210> 54

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> chemically synthesized

<400> 54

```

Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
  1                5                10                15
Ser His Leu Glu
        20

```